How Does the Public Discuss Gene Editing in Agriculture? An Analysis of Twitter Content

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Abstract

As people form their opinion about gene editing applications in agriculture, they are utilizing social media to seek and share information and opinions on the topic. Understanding how the public discusses this technology will influence the development of effective messaging and practitioner engagement in the conversation. The purpose of this study was to describe the characteristics of Twitter content related to applications of gene editing in agriculture. Social media monitoring facilitated a quantitative, descriptive analysis of public Twitter content related to the topic. A Meltwater social media monitor collected N = 13,189 relevant tweets for analysis, revealing the amount of conversation regarding gene editing in agriculture, the number of contributing Twitter users, and the reach of the conversation which was relatively stable over the life of the study. In contrast, engagement with the topic rose with the sentiment of tweets becoming increasingly positive. News organization accounts had the most reach while a mix of news accounts and personal accounts garnered the greatest engagement. These results demonstrate an opportunity for agricultural and science communicators to create affirmative messaging about gene editing in agriculture delivered through news media Twitter accounts potentially increasing the reach and engagement in the social system and with science communication.

Keywords

Diffusion of innovation, social media monitoring, Meltwater, social systems

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Introduction and Problem Statement

Stigmas, misrepresentations, and uproar characteristic of public opinion about genetically modified organisms could carry over to products of gene editing, hampering their potential to meet the challenge of global food demand (Rose et al., 2020; Shew et al., 2018). Science communicators and agriculturalists have an opportunity to stave off such negativity in favor of public appreciation for the complexities of the food system. To harness the potential, time is of the essence (Doxzen & Henderson, 2020; Wirz et al., 2020). Understanding how the public discusses gene editing applications in agriculture would help communicators develop strategies to promote the positive implications of the technology (Brossard, 2019; Wirz et al., 2020).

In general, gene-editing technologies are used for making specific improvements to desired traits in commercial plants and animals (Metje-Sprink et al., 2019). This technology is advantageous because of its superior speed, precision, accuracy, and cost (Metje-Sprink et al., 2019). Unlike genetic modification techniques, gene-editing technologies leave no detectable genetic material (Metje-Sprink et al., 2019). As Turnbull et al. (2021) states, "Scientists aver that gene editing is not 'genetic modification' because the method of introducing changes to the DNA is no different from changes that can occur during conventional breeding or in nature" (p. 3).

The increasing capabilities of gene editing elicit heightened visibility and conversation about the technology (Molteni, 2019). Such discussions take place, in part, online. Social media plays a significant role in viewing and sharing science information as 33% of Americans consider it an important way to get science news (Funk et al., 2017), with 69% getting news in general via Twitter (Mitchell et al., 2021). People who share information on social media want to shape a smart, helpful, and informed online identity (Kraft et al., 2020). People are more honest about their opinions on social media than they are in person (Varma et al., 2017).

Twitter is an excellent means for bridging and encouraging engagement between the public and science, but there is a need to understand how science is being discussed on the platform so communicators can improve platform-specific content (López-Goñi & Sánchez-Angulo, 2018). Previous research has examined Twitter users' perception of human applications of gene editing (Guertin et al., 2018), but a literature review did not find such research specific to agricultural applications. This study investigates how Twitter users are diffusing information regarding agricultural applications of gene editing through the social system of the platform.

Theoretical and Conceptual Framework

Diffusion of innovation theory served as the conceptual framework for this study. This theory posits members of a social system spread information about an innovation through two-way communication using various channels over time (Rogers, 2003). This study focuses on diffusion of information related to gene editing in agriculture through the social system of Twitter.

Science news is exchanged in this social environment to accomplish the common goal of demystifying the topic for the public (Busquet & Viken, 2019).

An individual becomes aware of the innovation, forms a perspective on it, decides whether to adopt or reject it, takes action on their decision, then seeks validation the right decision was made (Rogers, 2003). Social media use is increasingly used for knowledge sharing (Ahmed et al., 2019). Information perceived as useful and influential to others is more likely to be shared by social media users (Kraft et al., 2020). Research utilizing diffusion of innovation theory has found social media sharing behaviors indicate the sender's approval or acceptance of the information (Kee et al., 2016). The complexity and far-reaching social, health, economic, and national security implications of gene-editing technology make the innovation rife with uncertainty for many (Scheufele et al., 2017). With so many avenues of informational needs, people turn to multiple sources and communication channels, including social media and news media, to gather information to reduce their uncertainty (Rogers, 2003; Scheufele et al., 2017). When regulations, governmental guidance, and laws are established, uncertainty is reduced as availability of information increases about the technological characteristics and definitions of gene editing (Whelan et al., 2020). "It facilitates their decision process (Kat & Oomen, 2007) and the diffusion of innovation" (Whelan et al., 2020, p. 2).

Diffusion is affected by the norms and relationships within a social system (Rogers, 2003). Meng et al. (2018) utilized diffusion of innovation theory as a framework to identify mass media channels widely disseminate information via a tweet because of their large user following. Additionally, interpersonal connections serve as brokers to share information across communities. Tweets from brokers were retweeted by users more often, increasing the virality of the information (Meng et al., 2018). Zhu et al. (2020) also utilized diffusion of innovation theory to study tweets from the Center for Disease Control. Tweets with severity, efficacy, and call-for-action information were shared more rapidly and diffused to a greater number of receivers. In addition, tweets with a negative tone were shared faster and wider than positively toned tweets. Tweets with fewer affiliative words (e.g., ally, together, friend) were also shared more rapidly and to a greater number of receivers. The researchers concluded tweet characteristics have significant effects on diffusion outcomes (Zhu et al., 2020).

Siebert (2019) used diffusion of innovation theory in their framework to conduct a qualitative content analysis of tweets about the genetically-engineered AquAdvantage Salmon™. The author compared the themes of tweets from salmon producers and those from the public. They found producers focused on AquAdvantage Salmon™ as a solution to the complex food problem of meeting heightened demand for seafood while reducing environmental impact. Tweets from the public discussed how natural and safe the salmon was, as well as the need for proper labeling (Siebert, 2019). Siebert (2019) also included the characteristics of innovations (Rogers, 2003) as a means of explaining their findings regarding public hesitancy to accept AquAdvantage Salmon™.

Purpose

The purpose of this study was to describe the characteristics of Twitter content related to applications of gene editing in agriculture. The study was guided by the following research questions.

1. How many mentions of gene editing applications in agriculture were publicly posted on Twitter between September 1, 2018 and December 31, 2019?
2. What was the social reach and engagement of those tweets?
3. What was the sentiment of those tweets?
4. How does tweet reach and engagement vary based on tweet sentiment?

Methods

Social media monitoring was utilized to facilitate a quantitative, descriptive analysis of content related to gene editing applications in agriculture publicly posted on Twitter between September 1, 2018 and December 31, 2019. Data collection was not possible prior to September 1, 2018 as Meltwater only maintains a rolling 15 months of social media content. Collection concluded at the end of December 2019 due to the volume of tweets collected and the timeframe to complete the study.

Twitter is of particular interest for examining relationships within food systems as its structure and norms defy those of other social media platforms. The diverse usership able to view public accounts, and the continuous sharing of tweets disassemble audience boundaries to construct highly individual accounts contributing to the community at large (Pennell, 2016). According to the Pew Research Center (Wojcik & Hughes, 2019), approximately 22% of adult Americans use Twitter. The median age of a Twitter user is 40 years old, while the median age of a U.S. adult is 47 years old. Twitter users have slightly higher educational attainment than the general U.S. population, with 42% of adult Twitter users having bachelor's degree while 31% of the adult U.S. population has the same degree. Of adult Twitter users who reported their annual household income, 41% said it was higher than $75,000, while 31% of the general population's annual household income is above that dollar figure (Wojcik & Hughes, 2019). These characteristics, coupled with social media users' desire to portray an online identity that is smart, helpful, and informed, make Twitter users prime candidates to lead acceptance of new technologies (Berger, 2014; Boyd & Ellison, 2007; Rogers, 2003).

Meltwater, a social media monitoring platform, was used to collect the relevant content. A monitor was established within Meltwater using a Boolean search query (available upon request) to identify only content related to gene editing applications in agriculture within the designated time frame. The keywords included in the Meltwater monitor were based on an in-depth scan of the scholarly literature and popular press and the various terminology used to discuss gene editing therein (Huang et al., 2016; Johnson, 2015; Tagliabue, 2015; Guertin et al., 2018). Data were limited to the United States because definitions and regulations regarding gene editing differ from country to country (Metje-Sprink et al., 2019). The monitor gathered *N*

= 13,189 public tweets pertaining to the study, constrained by platform data limitations. IBM SPSS v. 25 was used for descriptive and non-parametric statistics to address the research questions. Statistical significance was set *a priori* at < .05 (Field, 2017).

Meltwater creates reports containing each tweet and extensive information associated with it, including the date and time the tweet was published, username of the publisher, full text of the tweet, country of origin, reach of the post (number of followers of the post author), engagement with the post if it is an original tweet (number of replies, retweets, and likes), and sentiment (overall positive, negative, or neutral tone) (Gan, 2021). Sentiment is analyzed by a Natural Language Processing Computational Linguistics algorithm to assess the opinion and emotions of a text and categorize it as positive, negative, or neutral in overall tone (Kadam & Joglekar, 2013; Bishop, n.d.).

Due to the nuanced, informal, and creatively punctuated nature of tweets, there is debate over the best method to mine sentiment from them (Roberts et al., 2018). To illuminate potential differences between manual and automated methods of sentiment analysis, the lead author manually annotated a randomly selected subset of 1% (n = 1,389) of the tweets from the sample (Roberts et al., 2018). Each tweet was read, then assigned into one of three categories (positive, negative, or neutral) based on the overall emotional tone of the tweet (Kadam & Joglekar, 2013; Roberts et al., 2018). Of the 1,389 tweets, 565 were annotated as positive, 363 as neutral, and 461 as negative in overall tone. Meltwater's natural language processing algorithm designated 570 tweets as positive, 146 as neutral, and 673 as negative. Overall, 951 (68.3%) of the subset tweets matched in sentiment assignment.

As examples of tweets the author and Meltwater agreed on in terms of sentiment: @InnovatureNow: Tailgating season is in full swing and thanks to agricultural innovations like gene editing, football food classics can stay in play. (positive); @HealthRanger: New Crispr GMO food is a dangerous experiment so don't be a lab rat that eats it! https://t.co/Fxi0zpYQua #crisprdanger #dangerousfood (negative); @CellBioNews170: Nature plants review explores the current state and future of CRISPR technology in crops https://t.co/zjkhQWmWJe (neutral).

While manual annotation allows a human to identify tone in a message and appreciate the sentiment of words in context, the subjectivity of the process in combination with the volume of tweets in need of coding are important limitations to this method of sentiment analysis (Resch et al., 2016; Roberts et al., 2018). Limitations are an inherent part of research. No social media monitoring tool or sentiment analysis algorithm is perfect, so platforms other than Meltwater should be used to assess differences in analysis. Meltwater was chosen for this study due to funding availability and application for practical use.

Findings

RQ1: How many mentions of gene editing applications in agriculture were publicly posted on Twitter between September 1, 2018, and December 31, 2019?
During the time frame of the study, there were 13,189 mentions of gene editing related to agriculture on Twitter that met the search criteria. Of those, 3,576 were posted in the last quarter of 2018 and 9,614 were posted in 2019. Those tweets were publicly posted by 5,824 unique users (individual accounts without duplication). Figure 1 displays the changes in frequency (or numerical count) of tweets and unique users contributing to the conversation by month during the search period for the study.

Figure 1

Frequency of Gene editing in Agriculture Tweets and Unique Twitter Users Contributing
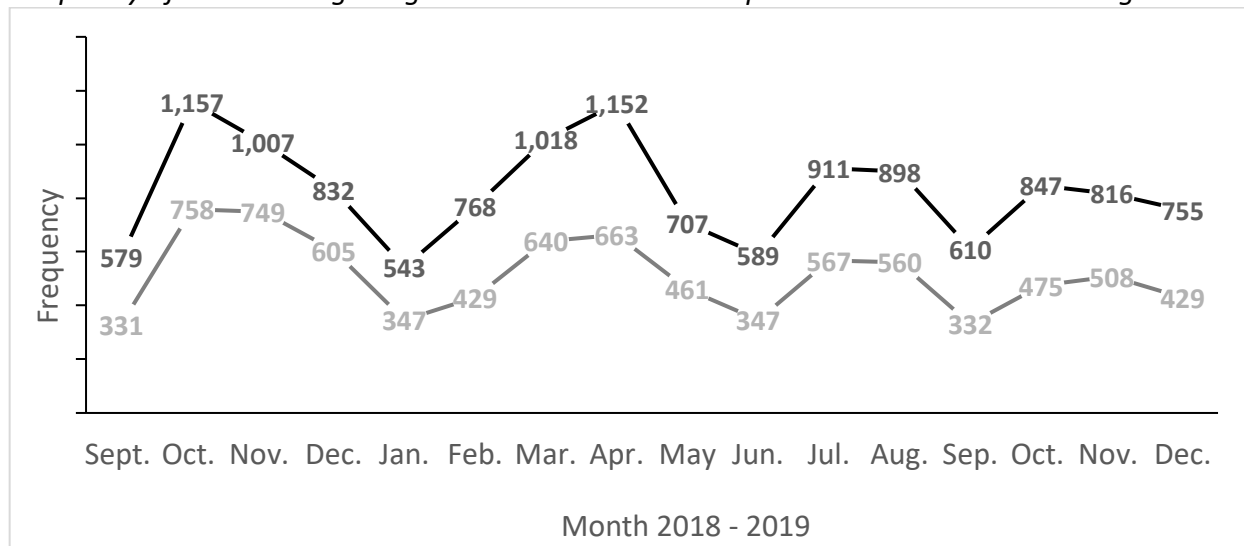

RQ2: What was the social reach and engagement of those tweets?
Tweets pertaining to the study had the potential to reach 266,554,740 Twitter users. Reach is the number of Twitter users who may see the tweet, calculated based on the number of followers of the post author (Gan, 2021). Peak reach occurred in May 2019 with 147,919,414 potential viewers of tweets regarding gene editing in agriculture. Figure 2 presents the changes in reach during the time period of the study.

Figure 2

Reach of Gene Editing in Agriculture Tweets
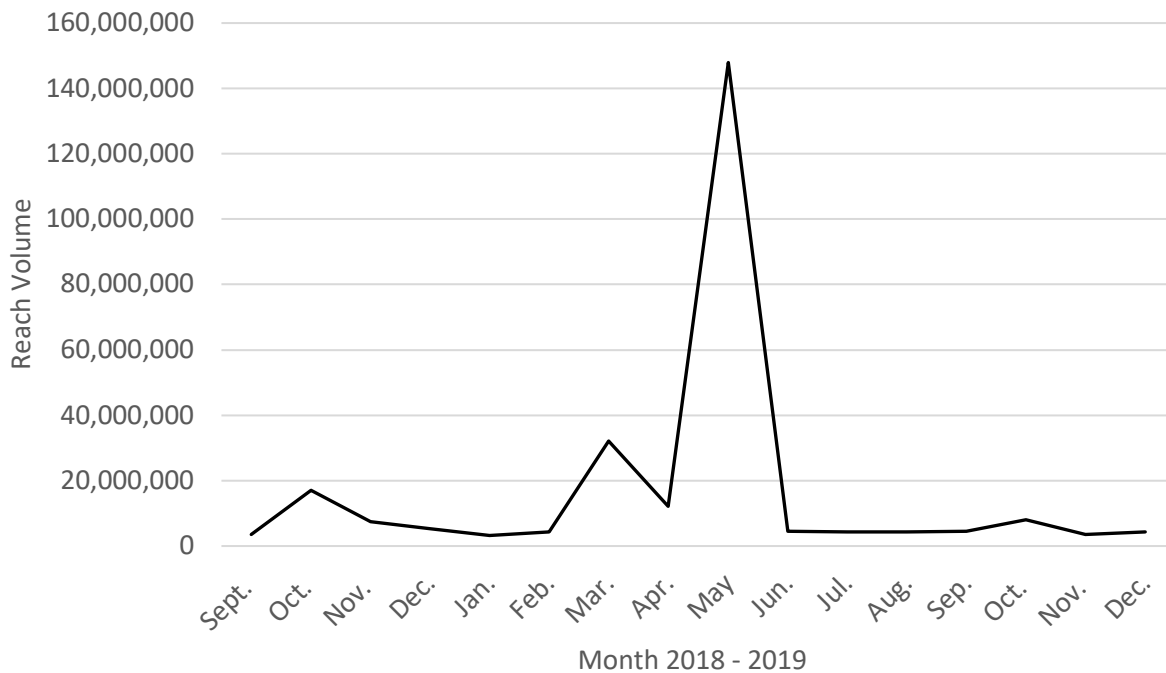
As the reach of a tweet is calculated based on the number of followers of the post author, the top 10 Twitter accounts in terms of reach are presented in Table 1.

Table 1

*Gene Editing in Agriculture Top 10 Twitter Accounts Regarding Reach*

Account Name	Account Type	Reach
nytimes	News Media	43,472,723
WIRED	News Media	10,349,781
ScienceNews	News Media	2,814,784
businessinsider	News Media	2,586,572
WIREDScience	News Media	2,013,565
TheAtlantic	News Media	1,828,854
CNET	News Media	1,621,044
sciencemagazine	News Media	1,246,320
NYTScience	News Media	1,150,285
RogueNASA	Personal Account	868,282

Original tweets pertaining to the study resulted in a total of 24,067 engagements, which are replies, retweets, and likes associated with an original tweet (Gan, 2021). Average engagement with individual tweets was 7.43 (*SD* = 17.69). Engagement with individual tweets ranged from

zero to 452. Figure 3 presents engagement with tweets and frequency of tweets during the time period of the study.

Figure 3

Frequency and Engagement with Gene Editing in Agriculture Tweets
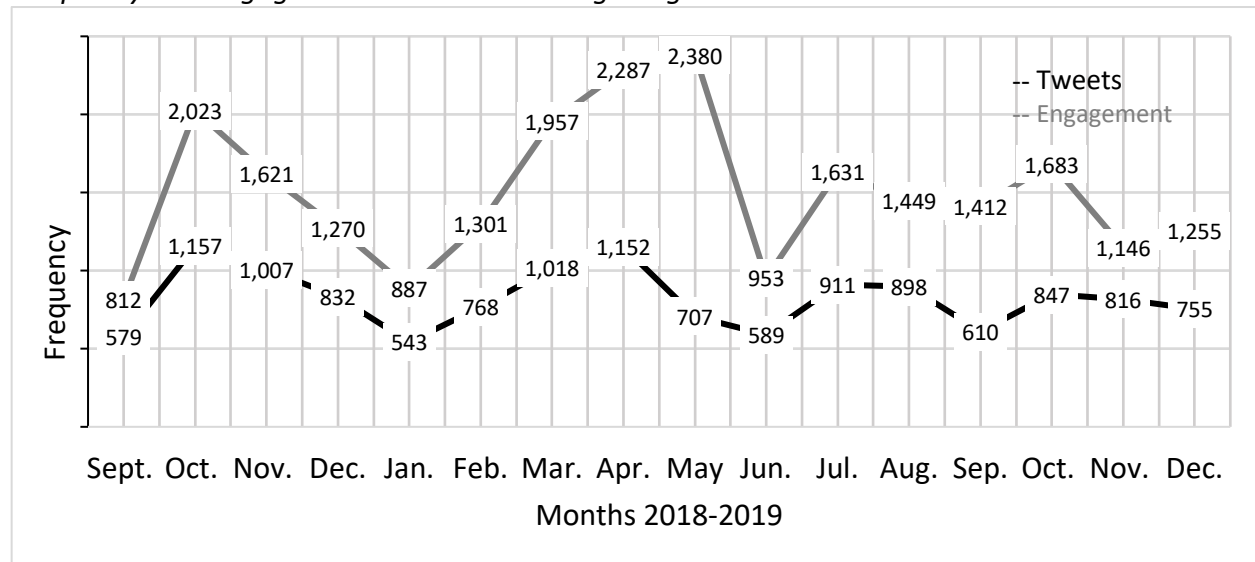
External to Meltwater's reporting, the proportion of retweets to original tweets was calculated as an indicator of interaction over the entire search (Grabbert et al., 2019). Of the 13,189 tweets collected, 7,022 (53.2%) were retweets, indicating high interaction among accounts participating in the conversation about gene editing in agriculture (Grabbert et al., 2019). The top 10 Twitter posts in terms of engagement are presented in Table 3.

Table 3

Gene Editing in Agriculture Top 10 Twitter Posts Regarding Engagement

| Account Name	Tweet	Engagement
ajitjohnson_n	Researchers used CRISPR before birth in an animal model to treat a lethal lung disease that causes death within hours after birth. This study shows that in utero editing could be a promising new approach for treating fatal diseases before birth. https://t.co/qqC4YeIUMo https://t.co/i1FtvMnwmz	452
nytimes	The world's first Crispr snails might help clear up a mystery of left/right asymmetry in the animal kingdom https://t.co/GwZxifW4CR	334

Account Name	Tweet	Engagement
nytimes	The world's first Crispr snails might help clear up a mystery of left/right asymmetry in the animal kingdom https://t.co/ptdPhaaSFt	320
nytimes	The world's first Crispr snails might help clear up a mystery of left/right asymmetry in the animal kingdom https://t.co/R3EIWOXcrL	243
Incarnated_ET	Scientists cure mice of HIV for first time in groundbreaking study using CRISPR A group of scientists have, for the first time, eliminated HIV DNA from the genomes of living animals, in what is being described as a critical step towards developing a cure for the AIDS virus.	209
AgBioWorld	Japan understands that gene-editing like #CRISPR is not GMO, just plain old mutagenesis with knowledge & precision! So, Genome-edited food products to go on sale in Japan, minus scary labelling or unnecessary regulatory burden https://t.co/VpbSW4PkMu	184
AgBioWorld	Whoa! A major breakthrough in sorghum, gene editing has elevated the protein of this important crop from 9-10% to a staggering 15-16%. Also improved digestibility. A big deal for Africa & India, another reason to embrace NBT, remove regulatory hurdles https://t.co/2WBlEECemA	165
IDSAInfo	Is #HIV a curable disease? A new study suggests yes, as researchers find success in eliminating the disease from an infected animal's genome through a combo of modified ARV treatment & gene-editing tool CRISPR-cas9. https://t.co/hrqZc4hATU #EndHIVEpidemic	122

Account Name	Tweet	Engagement
WIREDScience	Crispr works in almost every animal that scientists have tried, from silkworms to monkeys, and in just about every cell type—kidney cells, heart cells, you name it. What's more, Crispr is both fast and cheap. So how far do we want it to go? https://t.co/uueH6Bqbh0	121
BioBeef	So I binge watched #UnnaturalSelection on Netflix last night 'cause that is what animal geneticists with an interest in #scicomm do on a Friday night, & have some thoughts around agricultural applications of genome editing so I wrote a BLOG @ucanr @ucdavis https://t.co/pUb0jEPSC7	117

Note. Engagement is number of replies, retweets, and likes of an original tweet.

RQ3: What was the sentiment of those tweets?

Meltwater's natural language processing algorithm assigned a sentiment of positive, negative, or neutral to each tweet based on the overall tone of the message (Bishop, n.d.). Of all collected tweets (*N* = 13,189), Meltwater coded 5,083 (38.5%) as positive, 1,840 (14.0%) as negative, and 6,266 (47.5%) as neutral in tone. Peak positive sentiment occurred in November 2019 with 64% of tweets during the month having an overall positive tone. Peak negative sentiment occurred in February 2019, with 52% of tweets during the month having an overall negative tone. Peak neutral sentiment occurred in August 2019, with 62% of tweets during the month having an overall neutral tone. Figure 4 presents the sentiment of tweets during the time period of the study.

Figure 4

Sentiment of Gene Editing in Agriculture Tweets
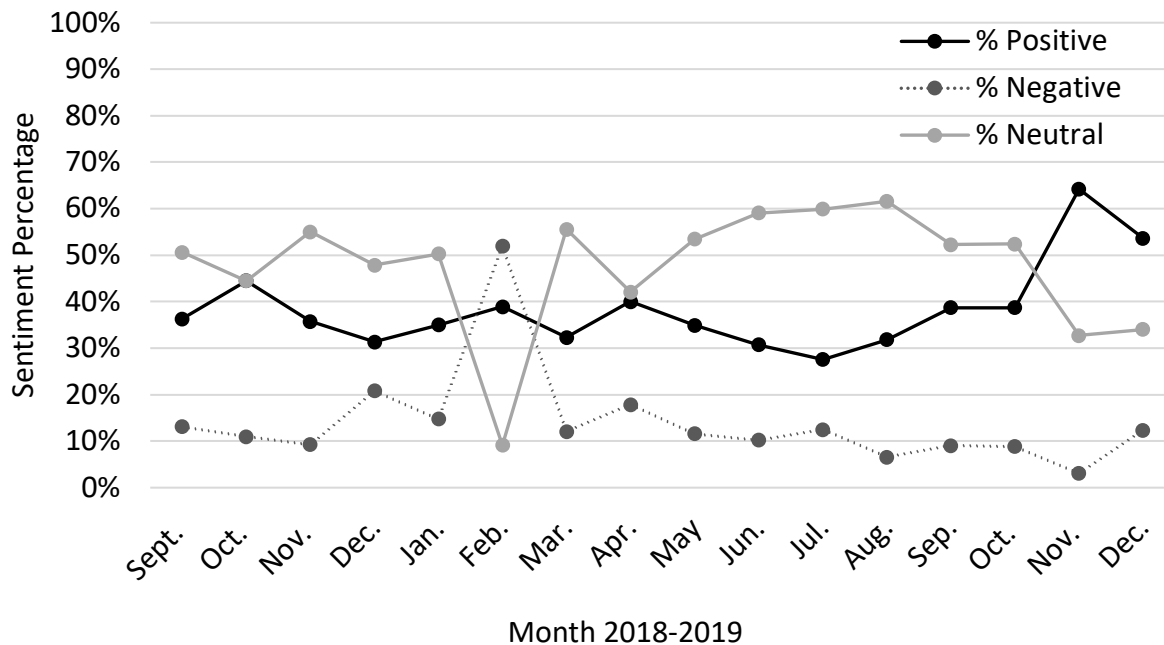
RQ4: How does tweet reach and engagement vary based on tweet sentiment?

A Kruskal-Wallis H test was utilized to address if tweet reach varied based on tweet sentiment, because a visual inspection of a boxplot indicated outliers too extreme to allow for ANOVA statistical analysis, but also too valuable to be removed from the data set (Field, 2017; Laerd Statistics, n.d.). As such, a Kruskal-Wallis H test was run to determine if there were differences in tweet reach between three groups of tweet sentiment: positive (n = 5,083), negative (n = 1,511), and neutral (n = 6,595). Distributions of reach were similar for all groups, as assessed by visual inspection of a boxplot, therefore requiring a comparison of medians (Laerd Statistics, n.d.). Median reach was statistically significantly different between groups, $\chi^2(2)$ = 8.279, p = .016. To determine differences between groups, pairwise comparisons were performed using Dunn's (1964) procedure with a Bonferroni correction for multiple comparisons. Adjusted p-values are presented. Post hoc analysis revealed statistically significant differences in median tweet reach between positive sentiment (Mdn = 944.00) and neutral sentiment (Mdn = 1011.00) tweets (p = .023), but not between positive sentiment and negative sentiment (Mdn = 915.00) (p = 1.00), or negative sentiment and neutral sentiment (p = .211).

To eliminate duplicated data, 7,022 retweets were removed from the population to focus on original tweet engagement. Additionally, 2,928 tweets received no replies, retweets, or likes, so these outliers were removed from the dataset in order to determine if a difference in sentiment elicits a difference in the amount of engagement. These steps left a sample of n = 3,239 tweets

for statistical analysis. A Kruskal-Wallis H test was utilized to address if tweet engagement varied based on tweet sentiment because a visual inspection of a boxplot indicated outliers too extreme to allow for ANOVA statistical analysis, but also too valuable to be removed from the data set (Field, 2017; Laerd Statistics, n.d.). As such, a Kruskal-Wallis H test was run to determine if there were differences in tweet engagement between three groups of tweet sentiment: positive (n = 1,285), negative (n = 417), and neutral (n = 1,537). Distributions of reach were not similar for all groups, as assessed by visual inspection of a boxplot, requiring a comparison of mean rank (Laerd Statistics, n.d.). Engagement was statistically significantly different between sentiment groups, $\chi^2(2)$ = 14.650, p = .001. To determine differences between groups, pairwise comparisons were performed using Dunn's (1964) procedure with a Bonferroni correction for multiple comparisons. Adjusted p-values are presented. Post hoc analysis revealed statistically significant differences in tweet engagement between positive sentiment (mean rank = 1696.15) and neutral sentiment (mean rank = 1573.77) tweets (p = .001), as well as between positive sentiment and negative sentiment (mean rank = 1555.75) (p = .021), but not negative sentiment and neutral sentiment (p = 1.00).

Conclusions, Discussion, and Recommendations

As people form their opinion about gene editing applications in agriculture, they turn to social media to seek and share information and opinions on the topic (Gil de Zúñiga, et al., 2012; Hughes et al., 2012). The associated sharing, liking, and tweeting behaviors mark the communication structure within the Twitter social system (Rogers, 2003). Communications strategies promoting the positive implications of gene editing applications in agriculture rest on an understanding of how the public discusses the technology (Brossard, 2019; Wirz et al., 2020).

Findings suggest Twitter users are marking their information exchange within the social system with increased participation in the form of replies, retweets, and likes as well as greater positivity (Kee et al., 2016; Rogers, 2003). This bodes well for the concern that negative public opinion of genetically modified organisms could carry over to products of gene editing (Rose et al., 2020; Shew et al., 2018).

As communicators will seek to expand the conversation about applications of gene editing, results indicate mass media channels hold the greatest opportunity to do so. All but one of the top 10 accounts with the greatest reach represent a news platform. Mass media channels, such as these, hold the greatest opportunity to influence knowledge acquisition about gene editing in agriculture by linking Twitter users to information outside of the social system (Rogers, 2003). Results indicated neutrally toned messages tended to reach a wider audience than positively toned tweets, but otherwise, there were no significant differences between sentiment and tweet reach. This result adds nuance to the findings of Zhu et al. (2020) who only examined reach of positive versus negative messages and found negative messages to be shared among a wider audience. Additional investigation of how the tone of tweets affects information diffusion is needed (Zhu et al., 2020).

Engagement with the conversation about gene editing can be an indicator of interaction among the social system as well as approval of or agreement with the message (Grabbert et al., 2019; Kee et al., 2016; Rogers, 2003). Both are goals among communicators who desire to create content that fosters conversation and encourages feedback from the audience. More than half of the tweets in this study were retweets. Higher engagement (a combination of retweets, replies and likes) was associated with positively toned tweets compared to negative or neutral tweets. This finding is in contrast with previous literature, which found negatively toned tweets to elicit higher engagement (Meng et al., 2018; Zhu et al., 2020). More investigation is needed, but our findings suggest as communicators seek to elicit engagement with content regarding gene editing in agriculture, they should consider creating messages with an optimistic or affirmative sentiment instead of fearful or indifferent tones.

Peaks and valleys in the datasets are cause for further inquiry into the information shared during a given month that received the greatest reach or engagement among the gene-editing in agriculture conversation on Twitter. A review of the top tweets in terms of reach and engagement by month reveal timely studies as well as policy speculation and updates regarding applications of gene-editing garner heightened attention. This suggests people are curious about gene-editing and also follow the regulatory journey of its applications.

In the future, researchers should consider a longitudinal study to see how characteristics of the Twitter discourse around gene editing in agriculture changes over time with the advancement and prevalence of the technology. Researchers should identify opinion leaders in gene editing to understand who may be driving the innovation-decision process among the public and across subsequent community networks.

To better understand public opinion of gene editing in agriculture, conversation about the topic could be monitored on other social media platforms as well as public opinion polls. A content analysis of the mass media channels on Twitter sharing information regarding gene editing in agriculture could give insight into what information readers are gathering about the topic. In addition, researchers should work with practitioners to develop and experimentally test messages with different sentiments to identify performance differences in a more controlled environment.

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